RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/534,130ASource: 10/534,130ADate Processed by STIC: 10/534,130A

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 05/23/2006
PATENT APPLICATION: US/10/534,130A TIME: 14:02:49

Input Set : A:\21415015.APP

Output Set: N:\CRF4\05232006\J534130A.raw

3 <110> APPLICANT: FRAZER, IAN HECTOR 5 <120> TITLE OF INVENTION: A METHOD FOR OPTIMISING GENE EXPRESSION USING SYNONYMOUS CODON OPTIMISATION 6 8 <130> FILE REFERENCE: 21415-0015US 10 <140> CURRENT APPLICATION NUMBER: 10/534,130A 11 <141> CURRENT FILING DATE: 2005-05-06 13 <150> PRIOR APPLICATION NUMBER: PCT/AU03/01487 14 <151> PRIOR FILING DATE: 2003-11-10 16 <150> PRIOR APPLICATION NUMBER: 60/425,163 17 <151> PRIOR FILING DATE: 2002-11-08 19 <160> NUMBER OF SEQ ID NOS: 126 21 <170> SOFTWARE: PatentIn version 3.3 23 <210> SEQ ID NO: 1 24 <211> LENGTH: 714 25 <212> TYPE: DNA 26 <213> ORGANISM: Artificial Sequence 28 <220> FEATURE: 29 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized GFP sequence 32 <220> FEATURE: 33 <221> NAME/KEY: CDS 34 <222> LOCATION: (1)..(711) 36 <400> SEQUENCE: 1 . 37 agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa 48 38 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu 41 ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt 96 42 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly 43 20 25 45 gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc 144 46 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 40 49 act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc tct 192 50 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser 55 53 tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat 240 54 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 70 57 gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc 288 58 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 90 '61 atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag 336

62 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys

Input Set : A:\21415015.APP

100					100													
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67																		384
69 ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat 432 70 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr 1		Pne	GIU		Asp	inr	Leu	vai		Arg	тте	GIU	ьeu	_	GIY	ше	Asp	
70 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr 1 130 135 140 137 136 ac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc 480 74 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile 51 145 150 160 77 aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag 78 Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln 79 165 170 175 181 ctg gcc gac cat tat caa cag ac act ccc atc ggc gac ggc cct gtg 82 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val 83 180 180 185 100 185 100 185 100 186 120 187 186 120 187 187 180 180 180 180 180 180 180 180 180 180													_4 -					420
11 130 135 140 140 148 140 140 140 140 140 140 140 140 140 140			-		-							_	_	~				432
73 acc tcc cac act gtg tac atc atg gcc gac acg cac acg cac acg act gcc acc acg cac acg act cac act tcc acg act acc acg acc acc act acc acg acc acc acc act gcc acc acc acc acc acc acc acc acc acc		Pne		GIU	Asp	GIY	ASI		Leu	GIY	HIS	гуѕ		GIU	Tyr	Asn	Tyr	
74 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile 75 145																		
155																		480
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79																		528
81 ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg 576 82 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Tle Gly Asp Gly Pro Val 83 180 185 190 185 190 85 ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa 624 86 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys 87 195 200 205 89 gat ccc aac gaa aag aga gac cac atg gtc ctg gag ttt gtg acc 672 90 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr 91 210 215 220 93 gct gcg gg atc aca cat ggc atg gac gag ctg tac aag tga 714 94 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 95 225 230 235 98 <210> SEQ ID NO: 2 99 <211> LENGTH: 237 100 <212> TYPE: PRT 101 <213> ORGANISM: Artificial Sequence 103 <220> FEATURE: 104 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized GFF sequence 107 <400> SEQUENCE: 2 108 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu 109 1 5 10 15 112 Leu Asp Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 117 35 40 45 120 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Lys Phe Ile Cys Thr 117 35 40 45 120 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser 121 50 55 124 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 125 65 126 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 127 65 132 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 133 100 105 90 136 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp		ьуѕ	vai	Asn	Pne	_	ıте	Arg	HIS	ASN		GIU	Asp	GIY	Ser		GIn	
82 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val 83 180 180 185 190 85 ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa 624 86 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys 87 195 200 205 87 200 205 88 gat ccc aac gaa aag aga gac cac atg gtc ctg ttg gag ttt gtg acc 672 90 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr 91 210 215 220 93 gct gct ggg atc ac act ggc atg gac gag ctg tac aag tga 714 94 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 95 225 230 235 98 <210> SEQ ID NO: 2 99 <211> LENGTH: 237 100 <212> TYPE: PRT 101 <213> ORGANISM: Artificial Sequence 103 <220> FEATURE: 104 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized GFP sequence 107 <400> SEQUENCE: 2 108 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu 109 1 109 1 5 10 15 112 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly 213 116 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 117 35 40 45 120 Thr Gly Lys Leu Pro Val Pro Thr Dro Thr Leu Lys Phe Ile Cys Thr 117 35 60 50 124 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 125 125 65 70 75 80 126 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 125 127 Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 125 128 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 129 85 90 95 132 Ile Phe Phe Lys Asp Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Lys Lys Lys Cys Cys Cys Cys Cys Cys Cys Cys Cys C																		
83																		576
85 ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa 624 86 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys 87 195 200 200 205 89 gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc 672 90 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr 215 200 215 220 210 215 220 210 210 215 220 214 93 gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 714 94 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 95 225 230 235 235 230 235 88 <210> SEQ ID NO: 2 99 <211> LENGTH: 237 100 <212> TYPE: PRT 101 <213> ORGANISM: Artificial Sequence 103 <220> FEATURE: 104 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized GFP sequence 107 <400> SEQUENCE: 2 108 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu 15 112 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly 13 20 25 30 116 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 17 35 40 45 120 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser 121 50 55 60 75 80 124 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 125 65 70 70 75 80 128 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 129 85 90 95 132 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 133 100 105 110		ьeu	Ala	Asp		ıyr	GIN	GIN	Asn		Pro	TTE	GIY	Asp	_	Pro	vaı	
86 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Āla Leu Ser Lys 87 195 200 205 88 gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc 672 90 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr 91 210 215 220 93 gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 714 94 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 95 225 230 235 98 <210> SEQ ID NO: 2 99 <211> LENGTH: 237 100 <212> TYPE: PRT 101 <213> ORGANISM: Artificial Sequence 103 <220> FEATURE: 104 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized GFP sequence 105 humanized GFP sequence 107 <400> SEQUENCE: 2 108 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu 109 1 5 10 15 112 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly 113 20 20 25 30 116 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys He Ile Cys Thr 17 35 40 40 18 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 19 1 50 75 80 124 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 19 1 65 90 95 132 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 13 100 105 105 105 105 110			a+ -															604
87																		624
89 gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc 672 90 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr 210 215 220 230 235 3 gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 714 94 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 95 225 230 235 98 <210 > SEQ ID NO: 2 99 <211 > LENGTH: 237		ьец	nea		Asp	ASII	птѕ	TAT		ser	IIII	GIII	ser		Leu	ser	гÀг	
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91		_			-	_	_	_		_	_	_	_					672
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109 1							ı Lev	. Phe	Thr	Glv	v Val	Val	Pro	o Ile	. Lei	ı Val	Glu	
112 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly 113			-	-						4								
113			ı Ası	Gly	Ast	Val	. Asr	Glv	His	Lvs	Phe	Ser	· Val	l Sei	Gly	7 Gli	ıGlv	
117			•	_	-			- 4		-					-		1	
117	116	Glu	Gly	Asp	Ala	Thr	Tyr	Glv	Lys	Leu	Thr	Leu	LVS	s Phe	: Ile	e Cvs	Thr	
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121 50 55 60 60 124 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 125 65 70 70 75 75 80 128 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 129 85 7 90 95 132 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 133 100 7 105 7 110 136 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			Gly	/ Lys	Leu	Pro	val	Pro	Trp	Pro	Thr	Lev	ı Val	l Thi	Thr	Phe	Ser	
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125 65 70 75 80 128 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 129 85 90 95 132 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 133 100 105 105 110 136 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp	124	Tyr	Gly	v Val	. Glr	Cys	. Phe	Ser	Aro	Tyr	Pro	Asp	His	Met	Lvs	Glr	n His	
128 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr 129			•			•			-	•					_			
129 85 90 95 132 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 133 100 105 110 136 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp	128	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	· Val	Glr	ı Glu	ı Arc		
132 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys 133 100 105 110 136 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp					•							•					•	
133 100 105 110 136 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp			Phe	Phe	Lys	Asr	Asp	Gly	Asn	Tyr	Lys	Thr	Arc	Ala	Glu		Lys	
136 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp								•					_	-			•	
			Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	. Le	ı Lys	Gly	, Ile	Asp	
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Input Set : A:\21415015.APP

Output Set: N:\CRF4\05232006\J534130A.raw

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Input Set : A:\21415015.APP

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250 1
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Input Set : A:\21415015.APP

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297 1
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316 1
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330 1
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342 <220> FEATURE:
343 <221> NAME/KEY: CDS
344 <222> LOCATION: (1)..(18)
346 <400> SEQUENCE: 13
347 cga cga cga cga cga
                                                                          18
348 Arg Arg Arg Arg Arg
```

VERIFICATION SUMMARY

DATE: 05/23/2006

PATENT APPLICATION: US/10/534,130A

TIME: 14:02:50

Input Set : A:\21415015.APP